

RAW SEQUENCE LISTING

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Application Serial Number: 09/879,312A
Source: IFW/6
Date Processed by STIC: 3-4-05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/09/879,312A

TIME: 15:08:12

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Output Set: N:\CRF4\03042005\I879312A.raw

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3 <110> APPLICANT: GLIMCHER, LAURIE H.
4     DOUHAN III, JOHN
6 <120> TITLE OF INVENTION: HUMAN C-MAF COMPOSITIONS AND METHODS OF USE THEREFOR
8 <130> FILE REFERENCE: HUI-027CPDV1
10 <140> CURRENT APPLICATION NUMBER: 09/879,312A
11 <141> CURRENT FILING DATE: 2001-06-12
13 <150> PRIOR APPLICATION NUMBER: 09/086,010
14 <151> PRIOR FILING DATE: 1998-05-27
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1203
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1203)
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32 1          5          10          15
34 ctg gcc atg gaa tat gtt aat gac ttc gat ctg atg aag ttt gaa gtg      96
35 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
36          20          25          30
38 aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt      144
39 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
40          35          40          45
42 ctc atc gcc ggg ggc tcg ctg tcc tcc acc ccc atg agc acg ccc tgc      192
43 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
44          50          55          60
46 agc tcg gtg ccc ccg tcc ccc agc ttc tcg gcg ccc agc ccg ggc tcg      240
47 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
48 65          70          75          80
50 cga ggc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc      288
51 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
52          85          90          95
54 tac ccg cag cag ctg aac ccc gag gcg ctg ggc ttc agc ccc gag gac      336
55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
56          100          105          110
58 gcg gtc gag gcg ctc atc agc aac agc cac cag ctc cgg ggc ggc ttc      384
59 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
60          115          120          125
62 gat ggc tat gcg cgc ggg gcg cag cag cta gcc gcg gcg gcc ggg gca      432

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63	Asp	Gly	Tyr	Ala	Arg	Gly	Ala	Gln	Gln	Leu	Ala	Ala	Ala	Ala	Gly	Ala	
64		130					135				140						
66	ggt	gcc	ggc	gcc	tcc	ttg	ggc	ggc	agc	ggc	gag	gag	atg	ggc	ccc	gcc	480
67	Gly	Ala	Gly	Ala	Ser	Leu	Gly	Gly	Ser	Gly	Glu	Glu	Met	Gly	Pro	Ala	
68	145					150					155					160	
70	gcc	gcc	gtg	gtg	tcc	gcc	gtg	atc	gcc	gcg	gcc	gcc	gcg	cag	agc	ggc	528
71	Ala	Ala	Val	Val	Ser	Ala	Val	Ile	Ala	Ala	Ala	Ala	Ala	Gln	Ser	Gly	
72					165					170						175	
74	gcg	ggc	ccg	cac	tac	cac	cac	cac	cac	cac	cac	gcc	gcc	ggc	cac	cac	576
75	Ala	Gly	Pro	His	Tyr	His	His	His	His	His	His	Ala	Ala	Gly	His	His	
76				180					185					190			
78	cac	cac	ccg	acg	gcc	ggc	gcg	ccc	ggc	gcc	gcg	ggc	agc	gcg	gcc	gct	624
79	His	His	Pro	Thr	Ala	Gly	Ala	Pro	Gly	Ala	Ala	Gly	Ser	Ala	Ala	Ala	
80			195					200					205				
82	tcg	gcc	ggt	ggc	gct	ggg	ggc	gcg	ggc	ggc	ggt	ggc	ccg	gcc	agc	gtt	672
83	Ser	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Gly	Gly	Pro	Ala	Ser	Val	
84		210					215					220					
86	ggg	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	gga	ggc	ggc	ggg	ggc	gcg	gcg	720
87	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala	
88	225					230					235					240	
90	ggc	gcc	ctg	cac	ccg	cac	cac	gcc	gcc	ggc	ggc	ctg	cac	ttc	gac	gac	768
91	Gly	Ala	Leu	His	Pro	His	His	Ala	Ala	Gly	Gly	Leu	His	Phe	Asp	Asp	
92				245						250					255		
94	cgc	ttc	tcc	gac	gag	cag	ctg	gtg	acc	atg	tct	gtg	cgc	gac	tgg	aac	816
95	Arg	Phe	Ser	Asp	Glu	Gln	Leu	Val	Thr	Met	Ser	Val	Arg	Asp	Trp	Asn	
96				260					265					270			
98	cgg	cag	ctg	cgc	ggg	gtc	agc	aag	gag	gag	gtg	atc	cgg	ctg	aag	cag	864
99	Arg	Gln	Leu	Arg	Gly	Val	Ser	Lys	Glu	Glu	Val	Ile	Arg	Leu	Lys	Gln	
100			275					280					285				
102	aag	agg	cgg	acc	ctg	aaa	aac	cgc	ggc	tat	gcc	aag	tcc	tgc	cgc	ttc	912
103	Lys	Arg	Arg	Thr	Leu	Lys	Asn	Arg	Gly	Tyr	Ala	Lys	Ser	Cys	Arg	Phe	
104		290					295					300					
106	aag	agg	gtg	cag	cag	aga	cac	gtc	ctg	gag	tcg	gag	aag	aac	cag	ctg	960
107	Lys	Arg	Val	Gln	Gln	Arg	His	Val	Leu	Glu	Ser	Glu	Lys	Asn	Gln	Leu	
108	305					310					315					320	
110	ctg	cag	caa	gtc	gac	cac	ctc	aag	cag	gag	atc	tcc	agg	ctg	gtg	cgc	1008
111	Leu	Gln	Gln	Val	Asp	His	Leu	Lys	Gln	Glu	Ile	Ser	Arg	Leu	Val	Arg	
112				325						330					335		
114	gag	agg	gac	gcg	tac	aag	gag	aaa	tac	gag	aag	ttg	gtg	agc	agc	ggc	1056
115	Glu	Arg	Asp	Ala	Tyr	Lys	Glu	Lys	Tyr	Glu	Lys	Leu	Val	Ser	Ser	Gly	
116				340					345					350			
118	ttc	cga	gaa	aac	ggc	tcg	agc	agc	gac	aac	ccg	tcc	tct	ccc	gag	ttt	1104
119	Phe	Arg	Glu	Asn	Gly	Ser	Ser	Ser	Asp	Asn	Pro	Ser	Ser	Pro	Glu	Phe	
120			355					360					365				
122	ttc	ata	act	gag	ccc	act	cgc	aag	ttg	gag	cca	tca	gtg	gga	tac	gcc	1152
123	Phe	Ile	Thr	Glu	Pro	Thr	Arg	Lys	Leu	Glu	Pro	Ser	Val	Gly	Tyr	Ala	
124		370					375					380					
126	aca	ttt	tgg	aag	ccc	cag	cat	cgt	gta	ctt	acc	agt	gtg	ttc	aca	aaa	1200
127	Thr	Phe	Trp	Lys	Pro	Gln	His	Arg	Val	Leu	Thr	Ser	Val	Phe	Thr	Lys	

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130 tga                                     1203
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144          20          25          30
146 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
147          35          40          45
149 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
150          50          55          60
152 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
153  65          70          75          80
155 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
156          85          90          95
158 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
159          100         105         110
161 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
162          115         120         125
164 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Gly Ala
165          130         135         140
167 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
168 145          150         155         160
170 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Gln Ser Gly
171          165         170         175
173 Ala Gly Pro His Tyr His His His His His Ala Ala Gly His His
174          180         185         190
176 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
177          195         200         205
179 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val
180          210         215         220
182 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
183 225          230         235         240
185 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
186          245         250         255
188 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
189          260         265         270
191 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
192          275         280         285
194 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
195          290         295         300
197 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
198 305          310         315         320
200 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
201          325         330         335

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203 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
204          340          345          350
206 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
207          355          360          365
209 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
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213 385          390          395          400
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219 <211> LENGTH: 1119
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221 <213> ORGANISM: Mus musculus
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (1)..(1119)
227 <400> SEQUENCE: 3
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230 1 5 10 15
232 ctg gcc atg gaa tat gtt aat gac ttc gat ctg atg aag ttt gaa gtg 96
233 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
234 20 25 30
236 aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt 144
237 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
238 35 40 45
240 ctc atc gcc ggg ggc tcg ctg tcc tcc acc ccc atg agc acg ccc tgc 192
241 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
242 50 55 60
244 agc tcg gtg ccc ccg tcc ccc agc ttc tcg gcg ccc agc ccg ggc tcg 240
245 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
246 65 70 75 80
248 ggc agc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc 288
249 Gly Ser Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
250 85 90 95
252 tac ccg cag cag ctc aac ccg gag gcg ctg ggc ttc agc ccg gag gac 336
253 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
254 100 105 110
256 gcg gtc gag gcg ctc atc agc aac agc cac cag ctc cag ggt ggc ttc 384
257 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Gln Gly Gly Phe
258 115 120 125
260 gat ggc tat gcg cgg gga gcg cag cag ctg gcc gcg gca gcg ggg gcc 432
261 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
262 130 135 140
264 ggc gcc ggc gcc tcc ctg ggc ggc agc ggc gag gag atg ggc ccc gcc 480
265 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
266 145 150 155 160
268 gcc gcc gtg gtg tcc gcc gtg atc gcc gcg gcc gcc gcg cag agc ggc 528
269 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly
270 165 170 175

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272 gcg gca ccc cac tac cat cac cac cac cac gcc gcg ggg cac cac 576
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276 cac cat ccg acg gcc ggc gcc ccg gga acc gcg ggc ggc gcg tct tcc 624
277 His His Pro Thr Ala Gly Ala Pro Gly Thr Ala Gly Gly Ala Ser Ser
278      195      200      205
280 tct tcg aac ggc gcg ggt ggc gcg ggc ggc ggt ggc ccg gcc aac acc 672
281 Ser Ser Asn Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Asn Thr
282      210      215      220
284 ggg ggc ggc ggc ggc gga gac ggc ggc ggc ggc acg gcg ggg gcg ggg 720
285 Gly Gly Gly Gly Gly Gly Asp Gly Gly Gly Gly Thr Ala Gly Ala Gly
286 225      230      235      240
288 ggc gcc ctt cac ccg cac cat tcc gcg ggc ggc ctg cac ttc gac gac 768
289 Gly Ala Leu His Pro His His Ser Ala Gly Gly Leu His Phe Asp Asp
290      245      250      255
292 cgc ttc tcg gac gag cag ttg gtg acc atg tcg gtg cgc gaa ctg aac 816
293 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Glu Leu Asn
294      260      265      270
296 cgg cag ctg cgc ggg gtc agc aag gag gag gtg atc cga ctg aag cag 864
297 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
298      275      280      285
300 aag agg cgg acc ctg aaa aac cgc ggc tat gcc cag tcc tgc cgc ttc 912
301 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Gln Ser Cys Arg Phe
302      290      295      300
304 aag agg gtg cag cag aga cac gtc ctg gag tcg gag aag aac cag ctg 960
305 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
306 305      310      315      320
308 ctg cag cag gta gac cac ctc aag cag gag atc tcc agg ctg gtg cgc 1008
309 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
310      325      330      335
312 gaa agg gac gcc tac aag gag aaa tac gag aag ctg gtg agc aac ggc 1056
313 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Asn Gly
314      340      345      350
316 ttc cga gaa aac ggc tcg agc agc gac aac cct tcc tct ccc gaa ttt 1104
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321 Phe Met
322      370
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330 <400> SEQUENCE: 4
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334 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
335      20      25      30
337 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg

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